

re-run

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/663,377
Source: 1Fwo
Date Processed by STIC: 9/25/03

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IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/663,377

DATE: 05/31/2005

TIME: 11:11:20

Input Set : N:\AMC\US10663377.raw
 Output Set: N:\CRF4\05312005\J663377.raw

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1 <110> APPLICANT: Liang, Yanbin
2      Woodward, David F.
3 <120> TITLE OF INVENTION: HUMAN COX-1 ALTERNATIVELY SPLICED
4      VARIANTS AND METHODS OF USING SAME
5 <130> FILE REFERENCE: 66872-028 (AR5746)
6 <140> CURRENT APPLICATION NUMBER: US/10/663,377
7 <141> CURRENT FILING DATE: 2003-09-15
8 <160> NUMBER OF SEQ ID NOS: 38
9 <170> SOFTWARE: FastSEQ for Windows Version 4.0
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 2022
13 <212> TYPE: DNA
14 <213> ORGANISM: Homo sapiens
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (298) . . . (2022)
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20 gtcctgctcg cggaccagg ggcccacg ccagggcct ctttgggagg aagccgcagg 120
21 caccaggaa aatgagttcc ctttccag cctctaaccg tctgggaacc catcctgatt 180
22 cccattgcca gtggagaagg tctccctgg tgaagacttc gggagaacat gggagatgga 240
23 aatacatatc ggagccggga tgcttcatct ggggttaag agatccccat tgagcaa atg 300
24                                         Met
25                                         1
26     agg aaa ccg agg ctc atg aat ccc tgt tgt tac tat cca tgc cag cac 348
27     Arg Lys Pro Arg Leu Met Asn Pro Cys Cys Tyr Tyr Pro Cys Gln His
28             5           10           15
29     cag ggc atc tgt gtc cgc ttc ggc ctt gac cgc tac cag tgt gac tgc 396
30     Gln Gly Ile Cys Val Arg Phe Gly Leu Asp Arg Tyr Gln Cys Asp Cys
31             20          25           30
32     acc cgc acg ggc tat tcc ggc ccc aac tgc acc atc cct ggc ctg tgg 444
33     Thr Arg Thr Gly Ser Gly Pro Asn Cys Thr Ile Pro Gly Leu Trp
34             35          40           45
35     acc tgg ctc cgg aat tca ctg cgg ccc agc ccc tct ttc acc cac ttc 492
36     Thr Trp Leu Arg Asn Ser Leu Arg Pro Ser Pro Ser Phe Thr His Phe
37             50          55           60           65
38     ctg ctc act cac ggg cgc tgg ttc tgg gag ttt gtc aat gcc acc ttc 540
39     Leu Leu Thr His Gly Arg Trp Phe Trp Glu Phe Val Asn Ala Thr Phe
40             70          75           80
41     atc cga gag atg ctc atg cgc ctg gta ctc aca gtg cgc tcc aac ctt 588
42     Ile Arg Glu Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn Leu
43             85          90           95
44     atc ccc agt ccc ccc acc tac aac tca gca cat gac tac atc agc tgg 636

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45	Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser Trp	
46	100 105 110	
47	gag tct ttc tcc aac gtg agc tat tac act cgt att ctg ccc tct gtg	684
48	Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser Val	
49	115 120 125	
50	cct aaa gat tgc ccc aca ccc atg gga acc aaa ggg aag aag cag ttg	732
51	Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln Leu	
52	130 135 140 145	
53	cca gat gcc cag ctc ctg gcc cgc ttc ctg ctc agg agg aag ttc	780
54	Pro Asp Ala Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe	
55	150 155 160	
56	ata cct gac ccc caa ggc acc aac ctc atg ttt gcc ttc ttt gca caa	828
57	Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala Gln	
58	165 170 175	
59	cac ttc acc cac cag ttc ttc aaa act tct ggc aag atg ggt cct ggc	876
60	His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro Gly	
61	180 185 190	
62	ttc acc aag gcc ttg ggc cat ggg gta gac ctc ggc cac att tat gga	924
63	Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile Tyr Gly	
64	195 200 205	
65	gac aat ctg gag cgt cag tat caa ctg cgg ctc ttt aag gat ggg aaa	972
66	Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly Lys	
67	210 215 220 225	
68	ctc aag tac cag gtg ctg gat gga gaa atg tac ccg ccc tcg gta gaa	1020
69	Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val Glu	
70	230 235 240	
71	gag gcg cct gtg ttg atg cac tac ccc cga ggc atc ccg ccc cag agc	1068
72	Glu Ala Pro Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln Ser	
73	245 250 255	
74	cag atg gct gtg ggc cag gag gtg ttt ggg ctg ctt cct ggg ctc atg	1116
75	Gln Met Ala Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu Met	
76	260 265 270	
77	ctg tat gcc acg ctc tgg cta cgt gag cac aac cgt gtg tgt gac ctg	1164
78	Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp Leu	
79	275 280 285	
80	ctg aag gct gag cac ccc acc tgg ggc gat gag cag ctt ttc cag acg	1212
81	Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln Thr	
82	290 295 300 305	
83	acc cgc ctc atc ctc ata ggg gag acc atc aag att gtc atc gag gag	1260
84	Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Glu	
85	310 315 320	
86	tac gtg cag cag ctg agt ggc tat ttc ctg cag ctg aaa ttt gac cca	1308
87	Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp Pro	
88	325 330 335	
89	gag ctg ctg ttc ggt gtc cag ttc caa tac cgc aac cgc att gcc atg	1356
90	Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala Met	
91	340 345 350	
92	gag ttc aac cat ctc tac cac tgg cac ccc ctc atg cct gac tcc ttc	1404
93	Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser Phe	

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Input Set : N:\AMC\US10663377.raw
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94	355	360	365	
95	aag gtg ggc tcc cag gag tac agc tac gag cag ttc ttg ttc aac acc			1452
96	Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn Thr			
97	370	375	380	385
98	tcc atg ttg gtg gac tat ggg gtt gag gcc ctg gtg gat gcc ttc tct			1500
99	Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe Ser			
100	390	395	400	
101	cgc cag att gct ggc cgg atc ggt ggg ggc agg aac atg gac cac cac			1548
102	Arg Gln Ile Ala Gly Arg Ile Gly Gly Arg Asn Met Asp His His			
103	405	410	415	
104	atc ctg cat gtg gct gtg gat gtc atc agg gag tct cgg gag atg cgg			1596
105	Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met Arg			
106	420	425	430	
107	ctg cag ccc ttc aat gag tac cgc aag agg ttt ggc atg aaa ccc tac			1644
108	Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr			
109	435	440	445	
110	acc tcc ttc cag gag ctc gta gga gag aag gag atg gca gca gag ttg			1692
111	Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu			
112	450	455	460	465
113	gag gaa ttg tat gga gac att gat gcg ttg gag ttc tac cct gga ctg			1740
114	Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu			
115	470	475	480	
116	ctt ctt gaa aag tgc cat cca aac tct atc ttt ggg gag agt atg ata			1788
117	Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile			
118	485	490	495	
119	gag att ggg gct ccc ttt tcc ctc aag ggt ctc cta ggg aat ccc atc			1836
120	Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile			
121	500	505	510	
122	tgt tct ccg gag tac tgg aag ccg agc aca ttt ggc ggc gag gtg ggc			1884
123	Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Glu Val Gly			
124	515	520	525	
125	ttt aac att gtc aag acg gcc aca ctg aag aag ctg gtc tgc ctc aac			1932
126	Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn			
127	530	535	540	545
128	acc aag acc tgt ccc tac gtt tcc ttc cgt gtg ccg gat gcc agt cag			1980
129	Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln			
130	550	555	560	
131	gat gat ggg cct gct gtg gag cga cca tcc aca gag ctc tga			2022
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133	565	570		
135	<210> SEQ ID NO: 2			
136	<211> LENGTH: 574			
137	<212> TYPE: PRT			
138	<213> ORGANISM: Homo sapiens			
139	<400> SEQUENCE: 2			
140	Met Arg Lys Pro Arg Leu Met Asn Pro Cys Cys Tyr Tyr Pro Cys Gln			
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142	His Gln Gly Ile Cys Val Arg Phe Gly Leu Asp Arg Tyr Gln Cys Asp			
143	20	25	30	

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144 Cys Thr Arg Thr Gly Tyr Ser Gly Pro Asn Cys Thr Ile Pro Gly Leu
145           35          40          45
146 Trp Thr Trp Leu Arg Asn Ser Leu Arg Pro Ser Pro Ser Phe Thr His
147           50          55          60
148 Phe Leu Leu Thr His Gly Arg Trp Phe Trp Glu Phe Val Asn Ala Thr
149           65          70          75          80
150 Phe Ile Arg Glu Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn
151           85          90          95
152 Leu Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser
153           100         105         110
154 Trp Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser
155           115         120         125
156 Val Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln
157           130         135         140
158 Leu Pro Asp Ala Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys
159           145         150         155         160
160 Phe Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala
161           165         170         175
162 Gln His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro
163           180         185         190
164 Gly Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile Tyr
165           195         200         205
166 Gly Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly
167           210         215         220
168 Lys Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val
169           225         230         235         240
170 Glu Glu Ala Pro Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln
171           245         250         255
172 Ser Gln Met Ala Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu
173           260         265         270
174 Met Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp
175           275         280         285
176 Leu Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln
177           290         295         300
178 Thr Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu
179           305         310         315         320
180 Glu Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp
181           325         330         335
182 Pro Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala
183           340         345         350
184 Met Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser
185           355         360         365
186 Phe Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn
187           370         375         380
188 Thr Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe
189           385         390         395         400
190 Ser Arg Gln Ile Ala Gly Arg Ile Gly Gly Arg Asn Met Asp His
191           405         410         415
192 His Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met

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193          420          425          430
194 Arg Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro
195          435          440          445
196 Tyr Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu
197          450          455          460
198 Leu Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly
199          465          470          475          480
200 Leu Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met
201          485          490          495
202 Ile Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro
203          500          505          510
204 Ile Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val
205          515          520          525
206 Gly Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu
207          530          535          540
208 Asn Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser
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210 Gln Asp Asp Gly Pro Ala Val Glu Arg Pro Ser Thr Glu Leu
211          565          570

213 <210> SEQ ID NO: 3
214 <211> LENGTH: 1818
215 <212> TYPE: DNA
216 <213> ORGANISM: Homo sapiens
217 <220> FEATURE:
218 <221> NAME/KEY: CDS
219 <222> LOCATION: (298)...(1620)
220 <400> SEQUENCE: 3
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223 caccaggaa aatgaggattcc ctttctccag cctctaaccg tctggaaacc catcttgatt 180
224 cccattgcca gtggagaagg tctccctgg tgaagacttc gggagaacat gggagatgga 240
225 aatacattta ggagccggga tgcttcatct ggggtttaag agatccccat tgagcaa atg 300
226                                         Met
227                                         1
228     agg aaa ccg agg ctc agg aag cag ttg cca gat gcc cag ctc ctg  348
229     Arg Lys Pro Arg Leu Arg Lys Gln Leu Pro Asp Ala Gln Leu Leu
230             5           10           15
231     gcc cgc cgc ttc ctg ctc agg agg aag ttc ata cct gac ccc caa ggc  396
232     Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe Ile Pro Asp Pro Gln Gly
233             20          25           30
234     acc aac ctc atg ttt gcc ttc ttt gca caa cac ttc acc cac cag ttc  444
235     Thr Asn Leu Met Phe Ala Phe Ala Gln His Phe Thr His Gln Phe
236             35          40           45
237     ttc aaa act tct ggc aag atg ggt cct ggc ttc acc aag gcc ttg ggc  492
238     Phe Lys Thr Ser Gly Lys Met Gly Pro Gly Phe Thr Lys Ala Leu Gly
239             50          55           60           65
240     cat ggg gta gac ctc ggc cac att tat gga gac aat ctg gag cgt cag  540
241     His Gly Val Asp Leu Gly His Ile Tyr Gly Asp Asn Leu Glu Arg Gln
242             70           75           80

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VERIFICATION SUMMARY

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Input Set : N:\AMC\US10663377.raw

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